

22828103	12725	22828104	12726	22828105	12727	22828106	12728	22828107	12729	22828108	12730	22828109	12731	22828110	12732	22828111	12733	22828112	12734	22828113	12735	22828114	12736	22828115	12737	22828116	12738	22828117	12739	22828118	12740	22828119	12741	22828120	12742	22828121	12743	22828122	12744	22828123	12745	22828124	12746	22828125	12747	22828126	12748	22828127	12749	22828128	12750	22828129	12751	22828130	12752	22828131	12753	22828132	12754	22828133	12755	22828134	12756	22828135	12757	22828136	12758	22828137	12759	22828138	12760	22828139	12761	22828140	12762	22828141	12763	22828142	12764	22828143	12765	22828144	12766	22828145	12767	22828146	12768	22828147	12769	22828148	12770	22828149	12771	22828150	12772	22828151	12773	22828152	12774	22828153	12775	22828154	12776	22828155	12777	22828156	12778	22828157	12779	22828158	12780	22828159	12781	22828160	12782	22828161	12783	22828162	12784	22828163	12785	22828164	12786	22828165	12787	22828166	12788	22828167	12789	22828168	12790	22828169	12791	22828170	12792	22828171	12793	22828172	12794	22828173	12795	22828174	12796	22828175	12797	22828176	12798	22828177	12799	22828180	12800	22828181	12801	22828182	12802	22828183	12803	22828184	12804	22828185	12805	22828186	12806	22828187	12807	22828188	12808	22828189	12809	22828190	12810	22828191	12811	22828192	12812	22828193	12813	22828194	12814	22828195	12815	22828196	12816	22828197	12817	22828198	12818	22828199	12819	22828200	12820	22828201	12821	22828202	12822	22828203	12823	22828204	12824	22828205	12825	22828206	12826	22828207	12827	22828208	12828	22828209	12829	22828210	12830	22828211	12831	22828212	12832	22828213	12833	22828214	12834	22828215	12835	22828216	12836	22828217	12837	22828218	12838	22828219	12839	22828220	12840	22828221	12841	22828222	12842	22828223	12843	22828224	12844	22828225	12845	22828226	12846	22828227	12847	22828228	12848	22828229	12849	22828230	12850	22828231	12851	22828232	12852	22828233	12853	22828234	12854	22828235	12855	22828236	12856	22828237	12857	22828238	12858	22828239	12859	22828240	12860	22828241	12861	22828242	12862	22828243	12863	22828244	12864	22828245	12865	22828246	12866	22828247	12867	22828248	12868	22828249	12869	22828250	12870	22828251	12871	22828252	12872	22828253	12873	22828254	12874	22828255	12875	22828256	12876	22828257	12877	22828258	12878	22828259	12879	22828260	12880	22828261	12881	22828262	12882	22828263	12883	22828264	12884	22828265	12885	22828266	12886	22828267	12887	22828268
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; GAP of: W0h051-7.Seg  check: 6926  from: 1  to: 52
```

seq of dicamba induced band w0c0 51.7

to: C:\lp181r.Seg check: 2737 from: 1 to: 714

Symbol comparison table: Gcgc core.Data.Rundata]Nwsgapdna.Cmp
CompCheck: 8760

Gap Weight:	50	Average Match:	10.000
Length Weight:	3	Average Mismatch:	0.000
Quality:	520	Length:	714
Ratio:	10.000	Gaps:	0
Percent Similarity:	100.000	Percent Identity:	100.000

Match display thresholds for the alignment(s):

IDENTITY

..
||
L

11.

W0h051-7.Seq x Cj1pi81r.Seq..

```

1  .....gctagctgcgcgctgaccacgcacat 26
   |||||
1  CGATCGAAGTGGTGTGTGCTAGCTAGCTGCGCGTGACCGCACAT 50
   |||||
27  gaccgcagtcgcgcggggtgatca..... 52
   |||||
51  GACCGCAGTGCGCCGGGGCTGATCAAGGGAAGTGATCGGATGGAGCTG 100

```

Figure 2

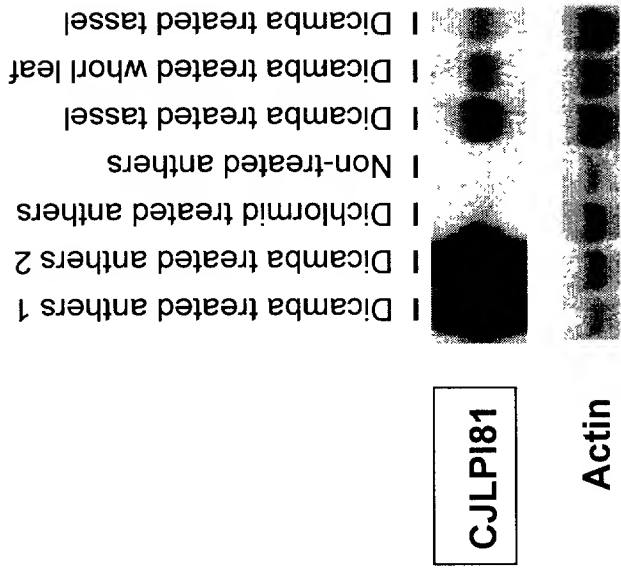


Figure 3

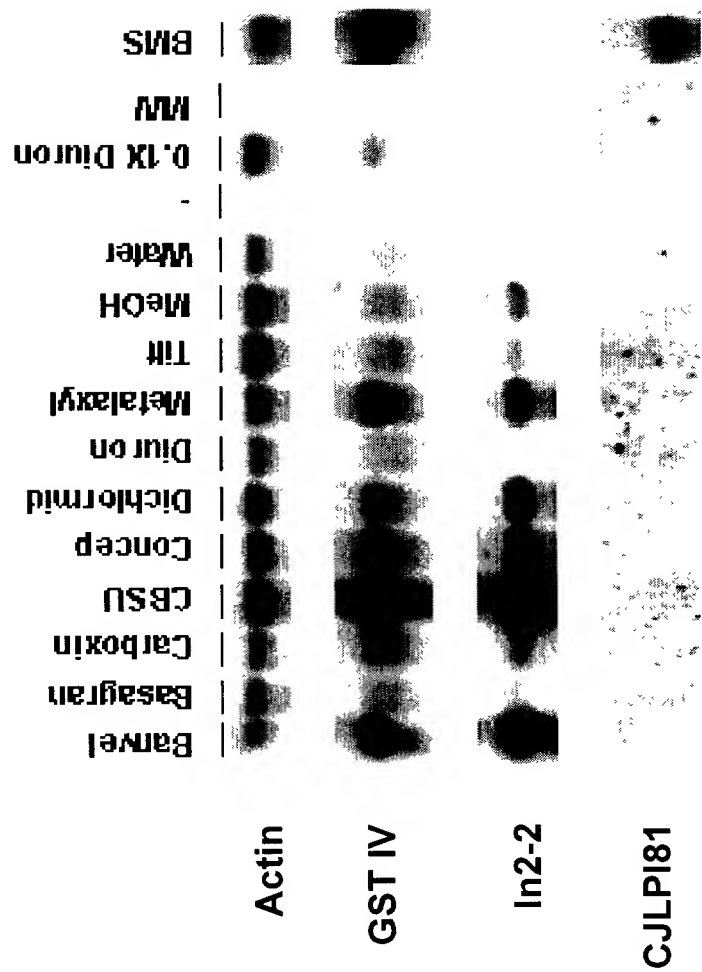


Figure 4

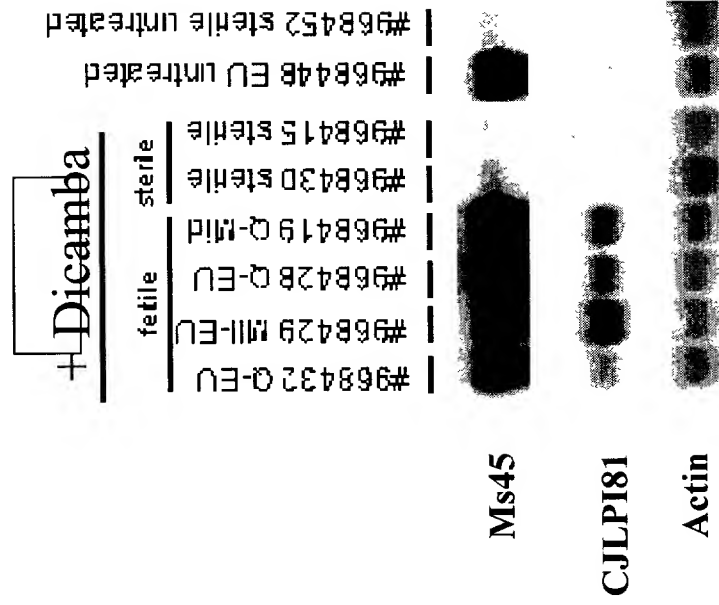


Figure 6

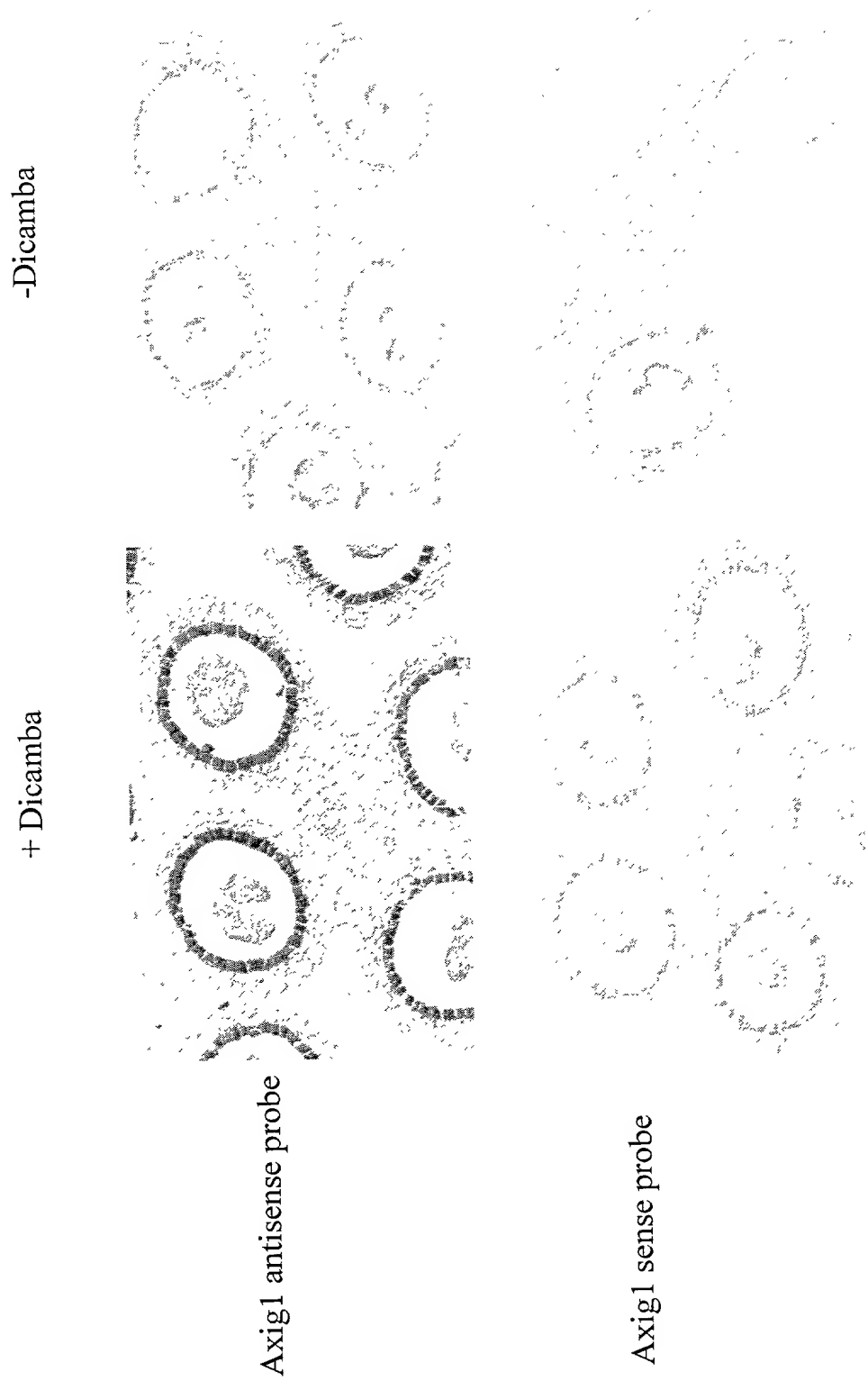


Figure 7

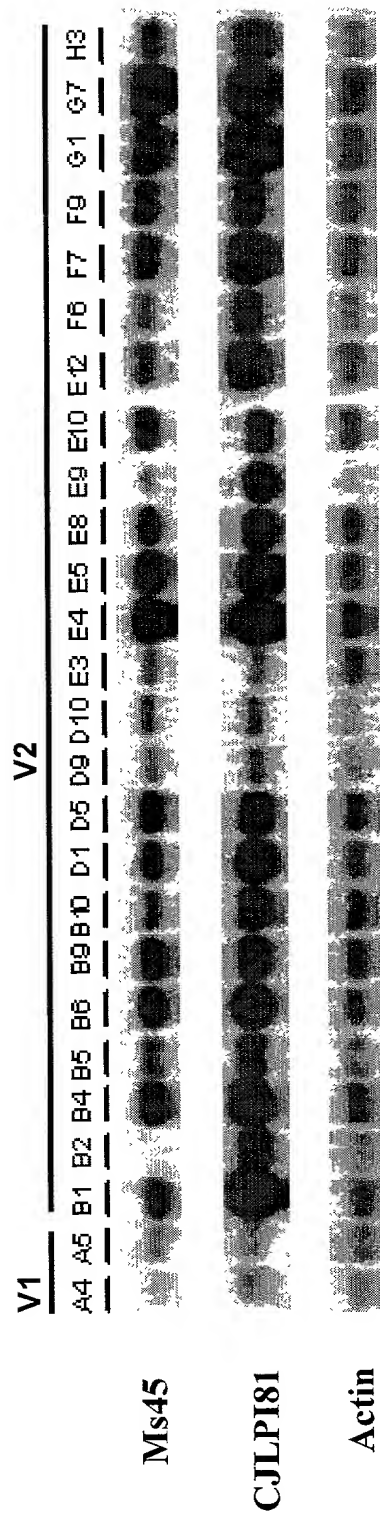


Figure 8

Figure 9

GAP of: Czaal47.Seq check: 446 from: 1 to: 1214
to: Axiglcomplete.Con check: 928 from: 1 to: 3123

Symbol comparison table:
Gencoredisk: [Gcgcore.Data.Rundata]Nwsgapdna.Cmp
CompCheck: 8760

Gap Weight: 50 Average Match: 10.000
Length Weight: 3 Average Mismatch: 0.000

Quality: 10871 Length: 3123
Ratio: 8.955 Gaps: 3
Percent Similarity: 100.000 Percent Identity: 100.000

Match display thresholds for the alignment(s):

| = IDENTITY
: = 5
. = 1

Czaal47.Seq x Axiglcomplete.Con May 11, 2000 12:05 ..

```

      .      .      .      .      .      .      .      .      .      .      .      .      .      .      .      .
1 .....GCAGGAACTTAT 12
      |||
1101 CGCGTCACTCACGGGTAGCTCATGGTCGAGCGTAGCATGCAGGAACTTAT 1150
      .      .      .      .      .      .      .      .      .      .      .      .      .      .      .      .
13 TTGCCGTGCGCTCCCAGGTCTCCGCTCGCGTGCCTTCCAGTCTGTCTCAC 62
      |||
1151 TTGCCGTGCGCTCCCAGGTCTCCGCTCGCGTGCCTTCCAGTCTGTCTCAC 1200
      .      .      .      .      .      .      .      .      .      .      .      .      .      .      .      .
63 ACTAGCTGCTGTGGGACGATCGAAGTGGGTGTGTTCAGCTAGCTAGCTGCG 112
      |||
1201 ACTAGCTGCTGTGGGACGATCGAAGTGGGTGTGTTCAGCTAGCTAGCTGCG 1250
      .      .      .      .      .      .      .      .      .      .      .      .      .      .      .      .
113 CCGTGACCACGCACATGACCGCAGTGCAGCGCGGGGCTGATCAAGGGAAAG 162
      |||
1251 CCGTGACCACGCACATGACCGCAGTGCAGCGCGGGGCTGATCAAGGGAAAG 1300
      .      .      .      .      .      .      .      .      .      .      .      .      .      .      .      .
163 TGATCGGATGGAGCTGGAGCTCGGGCTCGCGCCGCCGAACCCGCATCAGC 212
      |||
1301 TGATCGGATGGAGCTGGAGCTCGGGCTCGCGCCGCCGAACCCGCATCAGC 1350
      .      .      .      .      .      .      .      .      .      .      .      .      .      .      .      .
213 CGCTGGCTGCCGCCGCCGAGTTCGTTCGGTCTCCTCAGCAGCTCGGCTGGC 262
      |||
1351 CGCTGGCTGCCGCCGCCGAGTTCGTTCGGTCTCCTCAGCAGCTCGGCTGGC 1400
      .      .      .      .      .      .      .      .      .      .      .      .      .      .      .      .
263 TCGTGCGGGAACAAGAGGGTTCTCGGCGACGCGTTCGGGGCCGCCAAGGC 312
      |||
1401 TCGTGCGGGAACAAGAGGGTTCTCGGCGACGCGTTCGGGGCCGCCAAGGC 1450
      .      .      .      .      .      .      .      .      .      .      .      .      .      .      .      .
313 GGCCACGCTTCCGCTCTTCGTCTGCGAGGATGGCGACGGAGGCGGCGGCG 362
      |||
1451 GGCCACGCTTCCGCTCTTCGTCTGCGAGGATGGCGACGGAGGCGGCGGCG 1500

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363 ACCGCGACCGCGACGGCGTCGTCGACCATGAACAGCAAAGCAACAA.... 408
|||||
1501 ACCGCGACCGCGACGGCGTCGTCGACCATGAACAGCAAAGCAACAAGTGA 1550
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.
409 .....TGTACCCAGGAAGAAGAGGCTGG 431
|||||
1601 CCCAAATCCGATCCGTGGTGTGTAGTGTACCCAGGAAGAAGAGGCTGG 1650
.
.
432 TGGGGTGGCCCGCGGTGAAGTGC CGCGTAGGCGTAGCTGCGGCGGCGGG 481
|||||
1651 TGGGGTGGCCCGCGGTGAAGTGC CGCGTAGGCGTAGCTGCGGCGGCGGG 1700
.
.
482 TACGTGAAGGTGAAGCTGGAAGGGGTGCCCATCGGGCGGAAGGTGGACGT 531
|||||
1701 TACGTGAAGGTGAAGCTGGAAGGGGTGCCCATCGGGCGGAAGGTGGACGT 1750
.
.
532 GTCCATCCACGGCTCGTACCAGGAGCTGCTCCGCACGCTCGAGAGCATGT 581
|||||
1751 GTCCATCCACGGCTCGTACCAGGAGCTGCTCCGCACGCTCGAGAGCATGT 1800
.
.
582 TCCCTTCGGGTAACCAACA..... 600
|||||
1801 TCCCTTCGGGTAACCAACAAGGTGCGTACGTTCCCGGGCCGCGGCGAGCC 1850
.
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.
601 .....AG 602
||
1951 CTCCCGGCACTTAACTTGGTCGCATATACTATTCTGTAACTCTGGCAG 2000
.
.
603 ATCATGCAGAAGACGAGGTGGTGGTCTCGCACGAGCGCCCGCTCGCCAT 652
|||||
2001 ATCATGCAGAAGACGAGGTGGTGGTCTCGCACGAGCGCCCGCTCGCCAT 2050
.
.
653 CCTTATGTAGTCACCTACGAGGACGGCGAAGGGGACTGGTTGCTCGTCGG 702
|||||
2051 CCTTATGTAGTCACCTACGAGGACGGCGAAGGGGACTGGTTGCTCGTCGG 2100
.
.
703 AGATGATGTGCCGTGGGA..... 720
|||||
2101 AGATGATGTGCCGTGGGAGTACGTATCAGTCACTACTACTGTCGTCGTGTA 2150
.
.
.
721 .....GGTCTTTGTCAAGTCAGTG 739
|||||
2201 GAACTTAAAAACGACGTTGATTTCTTGCAGGGTCTTTGTCAAGTCAGTG 2250
.
.
740 AAGCGGCTCAAGATACTTGCGTAGCCGACGGTCGGCGCCTCAGAGACGTC 789
|||||
2251 AAGCGGCTCAAGATACTTGCGTAGCCGACGGTCGGCGCCTCAGAGACGTC 2300

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790 GTGTGGTCCGTCTCACCAGGATCGGAGCAGTGTAGTACTCCTGGGCGTCA 839
    |||||||||||||||||||||||||||||||||||||||||||||||
2301 GTGTGGTCCGTCTCACCAGGATCGGAGCAGTGTAGTACTCCTGGGCGTCA 2350

840 TCTGCGTAATAACGTTGTTTCTGTCCTGTGTGCCCCGTAGCAGTACGTACT 889
    |||||||||||||||||||||||||||||||||||||||||||||||
2351 TCTGCGTAATAACGTTGTTTCTGTCCTGTGTGCCCCGTAGCAGTACGTACT 2400

890 GTCCTATAGTAAGCTAGCTTTATGGGGTGCTTCAGCTTTCAGAGCATGAC 939
    |||||||||||||||||||||||||||||||||||||||||||||||
2401 GTCCTATAGTAAGCTAGCTTTATGGGGTGCTTCAGCTTTCAGAGCATGAC 2450

940 GAAAGCACTGATTAGCTGCTGTCATCACATTTGGTTTCGTCTTTGTGTCGT 989
    |||||||||||||||||||||||||||||||||||||||||||||||
2451 GAAAGCACTGATTAGCTGCTGTCATCACATTTGGTTTCGTCTTTGTGTCGT 2500

990 ACGGTATCGCTGGCGTCAGTGTGCGGGCAGCCTAGGTGATCTAAGCATAC 1039
    |||||||||||||||||||||||||||||||||||||||||||||||
2501 ACGGTATCGCTGGCGTCAGTGTGCGGGCAGCCTAGGTGATCTAAGCATAC 2550

1040 TTACTATCTCAAGTTACTTTTGGTTTCTTGAGCTTGCATGGTAATTCATA 1089
    |||||||||||||||||||||||||||||||||||||||||||||||
2551 TTACTATCTCAAGTTACTTTTGGTTTCTTGAGCTTGCATGGTAATTCATA 2600

1090 TACCGTATACGTGTGTGACTCAGGGGCGAAGCTGCCTTAAGGCACAGGGG 1139
    |||||||||||||||||||||||||||||||||||||||||||||||
2601 TACCGTATACGTGTGTGACTCAGGGGCGAAGCTGCCTTAAGGCACAGGGG 2650

1140 TCACCGGACCCGATGGAATTTATCAAATCCAGTGTAATAACTATTTAAC 1189
    |||||||||||||||||||||||||||||||||||||||||||||||
2651 TCACCGGACCCGATGGAATTTATCAAATCCAGTGTAATAACTATTTAAC 2700

1190 ACTGTTTCATCAATATATTTGATTTT..... 1214
    |||||||||||||||||||||||
2701 ACTGTTTCATCAATATATTTGATTTCAATAATTCATGGAGCTGACCTTGTG 2750

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 .
 .

Sequence Name	SEQ ID NO:	ATCC Deposit
Pioneer clone CZAAL47	1	PTA-2426
ZmAxig1 polypeptide	2	
Native ZmAxig1 promoter region	3	
Modified ZmAxig1 promoter region	4	PTA-2427
A632 full-length ZmAxig1, including SEQ ID No. 3	5	PTA-2426 PTA-2427
Primer 1, used for isolation of 5' flanking region	6	
Primer 2, used for isolation of 5' flanking region	7	
Primer 3, used for isolation of region spanning start codon	8	
Primer 4, used for isolation of region spanning start codon	9	
Primer 5, used for isolation of 5' region	10	
Oligonucleotide designed to remove clones having a poly-A tail but no cDNA	11	
Pioneer clone Cjlp181	12	
CuraGen fragment w0h051.7	13	
Primer 6, used to isolate the coding sequence and 3' region	14	
Primer 7, used to isolate the coding sequence and 3' region	15	
Modified ZmAxig1 promoter region with single-base deletion	16	PTA-2427
LEC1 transcriptional activator element	17	
LEC1 polynucleotides	18-20	
LEC1 polypeptide consensus sequence	21	

Figure 10. Representative polynucleotides and polypeptides of the present invention.

Experiment	Control	Ubi:LEC1	Axig1:LEC1
#1 3938.37	15%	63%	44%
#2 3938.79	4%	17%	20%
#3 3938.78	16%	17%	38%
#4 3938.34	2%	14%	13%

Figure 11. Transformation frequencies by LEC1 with two different promoters. Transformation frequencies were based on the percentage of plated embryos with one or more GFP positive/Bialaphos resistant colonies. All embryos were shot with Ubi:moPAT~GFP (a construct conferring Bialaphos resistance and GFP fluorescence) along with a LEC1 construct or a control DNA.